



-1-

SEQUENCE LISTING

RECEIVED
OCT 11 2001
TECH CENTER 1600/2300

<110> CURAGEN CORPORATION
RASTELLI, LUKA

<120> WNT-REGULATED CYTOKINE-LIKE POLYPEPTIDE AND NUCLEIC
ACIDS ENCODING SAME

<130> 10716/12

<140> 09/715,418

<141> 2000-11-16

<150> 60/166,177

<151> 1999-11-18

<160> 48

<170> PatentIn Ver. 2.1

<210> 1

<211> 212

<212> DNA

<213> Mus sp.

<400> 1

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<210> 2

<211> 1670

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<213> Mus sp.

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<221> modified_base

<222> (1541)

<223> "n" represents a, t, c, g, other or unknown

<400> 2

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<210> 3

<211> 131

<212> PRT

0213> Mus sp.

0400> 3

Ser Ile Ser Ser Cys Gly Ala Gly Tyr Arg Thr Asp Asp Lys Thr Gln

1 5 10 15

Leu Thr Glu Gly Arg Thr Ser Val Pro Gly Thr Met Gly Gln Cys Arg

20 25 30

Ser Ala Asn Ala Glu Asp Ala Gln Glu Phe Ser Asp Val Glu Arg Ala

35 40 45

Ile Glu Thr Leu Ile Lys Asn Phe His Lys Tyr Ser Val Ala Gly Lys

50 55 60

Lys Glu Thr Leu Thr Pro Ala Glu Leu Arg Asp Leu Val Thr Gln Gln

65 70 75 80

Leu Pro His Leu Met Pro Ser Asn Cys Gly Leu Glu Glu Lys Ile Ala

85 90 95

Asn Leu Gly Asn Cys Asn Asp Ser Lys Leu Glu Phe Gly Ser Phe Trp

100 105 110

Glu Leu Ile Gly Glu Ala Ala Lys Ser Val Lys Met Glu Arg Pro Val

115 120 125

Thr Arg Ser

130

0210> 4

0211> 357

0212> DNA

0213> Homo sapiens

0220>

0221> modified_base

<222> (231)

<223> "n" represents a, t, c, g, other or unknown

<220>

<221> modified_base

<222> (337)

<223> "n" represents a, t, c, g, other or unknown

<400> 4

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catcaagaa cttcaccagt actccgtgga ggggtgggaag gagacgctga ccccttctga 180
gtacggggac ctggtcaccc agcagctgcc ccattctcat ccgagcaact ntggcctgga 240
agagaaaatt gccaacctgg gcagctgcaa tgactctaaa ctggagttca ggagtttctg 300
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<211> 379

<212> DNA

<213> Homo sapiens

<400> 5

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caggttggca attttctctt ccaggccaca gttgctcggc atgagatggg gcagctgctg 180
ggtagaccagg tcccgtagct cagaaggggt cagcgtctcc ttcccacct ccacggagta 240
ctgggtgaaag ttcttgatga gggctcfaat ggccctctcc acatcactga attcctgagc 300
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<210> 6

<211> 118

<212> PRT

<213> Homo sapiens

<400> 6

Asp Asn Arg Thr Leu Thr Lys Gly Pro Asp Thr Val Ser Thr Met Gly
1 5 10 15

Gln Cys Arg Ser Ala Asn Ala Glu Asp Ala Gln Glu Phe Ser Asp Val
20 25 30

Glu Arg Ala Ile Glu Thr Leu Ile Lys Asn Phe His Gln Tyr Ser Val
35 40 45

Glu Gly Gly Lys Glu Thr Leu Thr Pro Ser Glu Leu Arg Asp Leu Val
50 55 60

Thr Gln Gln Leu Pro His Leu Met Pro Ser Asn Cys Gly Leu Glu Glu
65 70 75 80

Lys Ile Ala Asn Leu Gly Ser Cys Asn Asp Ser Lys Leu Glu Phe Arg
85 90 95

Ser Phe Trp Glu Leu Ile Gly Glu Ala Ala Lys Ser Val Lys Leu Glu
100 105 110

Arg Pro Val Arg Gly His
115

<210> 7

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 7

attgatgagg gtctcaatgg

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<210> 8

<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Probe

<400> 8
ccacatcact gaattcctga gcatcc 26

<210> 9
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 9
cagacacagt gaggaccatg 20

<210> 10
<211> 98
<212> PRT
<213> Homo sapiens

<400> 10
Met Ala Ala Glu Pro Leu Thr Glu Leu Glu Glu Ser Ile Glu Thr Val
1 5 10 15
Val Thr Thr Phe Phe Thr Phe Ala Arg Gln Glu Gly Arg Lys Asp Ser
20 25 30
Leu Ser Val Asn Glu Phe Lys Glu Leu Val Thr Gln Gln Leu Pro His
35 40 45

Leu Leu Lys Asp Val Gly Ser Leu Asp Glu Lys Met Lys Ser Leu Asp
50 55 60

Val Asn Gln Asp Ser Glu Leu Lys Phe Asn Glu Tyr Trp Arg Leu Ile
65 70 75 80

Gly Glu Leu Ala Lys Glu Ile Arg Lys Lys Lys Asp Leu Lys Ile Arg
85 90 95

Lys Lys

0210 11

0211 110

0212 PRT

0213 Homo sapiens

0400 11

Met Ser Gln Leu Glu Arg Asn Ile Glu Thr Ile Ile Asn Thr Phe His
1 5 10 15

Gln Tyr Ser Val Lys Leu Gly His Pro Asp Thr Leu Asn Gln Gly Glu
20 25 30

Phe Lys Glu Leu Val Arg Lys Asp Leu Gln Asn Phe Leu Lys Lys Glu
35 40 45

Asn Lys Asn Glu Lys Val Ile Glu His Ile Met Glu Asp Leu Asp Thr
50 55 60

Asn Ala Asp Lys Gln Leu Ser Phe Glu Glu Phe Ile Met Leu Met Ala
65 70 75 80

Arg Leu Thr Trp Ala Ser His Glu Lys Met His Glu Gly Asp Glu Gly
85 90 95

Pro Gly His His His Lys Pro Gly Leu Gly Glu Gly Thr Pro

100

105

110

<210> 12

<211> 37

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: 3-100/ICaBP type
calcium binding protein

<400> 12

Ser Asn Cys Gly Leu Glu Glu Lys Ile Ala Asn Leu Gly Ser Cys Asn

1

5

10

15

Asp Ser Lys Leu Glu Phe Arg Ser Phe Trp Glu Leu Ile Gly Glu Ala

20

25

30

Ala Lys Ser Val Lys

35

<210> 13

<211> 37

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: 3-100/ICaBP type
calcium binding protein

<400> 13

Asp Val Glu Arg Ala Ile Glu Thr Leu Ile Lys Asn Phe His Gln Tyr

1

5

10

15

Ser Val Glu Gly Gly Lys Glu Thr Leu Thr Pro Ser Glu Leu Arg Asp

20

25

30

Leu Val Thr Gln Gln

35

210 14

211 19

212 PFT

213 Unknown Organism

220

223 Description of Unknown Organism: Bacterial type II
secretion system protein F

400 14

Val Thr Gln Gln Leu Pro His Leu Met Pro Ser Asn Cys Gly Leu Glu

1

5

10

15

Glu Lys Ile

210 15

211 10

212 PFT

213 Unknown Organism

220

223 Description of Unknown Organism: Ubiquitin
carboxyl-terminal hydrolases family

400 15

Ala Asn Ala Glu Asp Ala Gln Glu Phe Ser

1

5

10

210 16

211 49

•212• PRT

•213• Unknown Organism

•220•

•223• Description of Unknown Organism: Bacterial
themotaxis sensory transducers protein

•400• 16

Gly Gly Lys Glu Thr Leu Thr Pro Ser Glu Leu Arg Asp Leu Val Thr
1 5 10 15

Gln Gln Leu Pro His Leu Met Pro Ser Asn Cys Gly Leu Glu Glu Lys
20 25 30

Ile Ala Asn Leu Gly Ser Cys Asn Asp Ser Lys Leu Glu Phe Arg Ser
35 40 45

Phe

•210• 17

•211• 32

•212• PRT

•213• Unknown Organism

•220•

•223• Description of Unknown Organism:
Phosphoenolpyruvate carboxykinase (ATP) protein

•400• 17

Met Gly Gln Cys Arg Ser Ala Asn Ala Glu Asp Ala Gln Glu Phe Ser
1 5 10 15

Asp Val Glu Arg Ala Ile Glu Thr Leu Ile Lys Asn Phe His Gly Tyr
20 25 30

•210• 18

<211> 33

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Prokaryotic-type
carbonic anhydrases proteins

<400> 18

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| His | Gln | Tyr | Ser | Val | Glu | Gly | Gly | Lys | Glu | Thr | Leu | Thr | Pro | Ser | Glu |
| 1 | | | | 5 | | | | 10 | | | | | 15 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Arg | Asp | Leu | Val | Thr | Gln | Gln | Leu | Pro | His | Leu | Met | Pro | Ser | Asn |
| | 20 | | | | | | 25 | | | | | 30 | | | |

Cys

<210> 19

<211> 15

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Ergosterol
biosynthesis ERG4/ERG24 family protein

<400> 19

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Ala | Asn | Leu | Gly | Ser | Cys | Asn | Asp | Ser | Lys | Leu | Glu | Phe | Arg |
| 1 | | | 5 | | | | | 10 | | | | 15 | | |

<210> 20

<211> 25

<212> PRT

<213> Unknown Organism

<220>

•223• Description of Unknown Organism:

Lysosome-associated membrane glycoproteins du

•400• 20

Leu Met Pro Ser Asn Cys Gly Leu Glu Glu Lys Ile Ala Asn Leu Gly

1

5

10

15

Ser Cys Asn Asp Ser Lys Ile Glu Phe

20

25

•210• 31

•211• 39

•212• PRT

•213• Unknown Organism

•220•

•223• Description of Unknown Organism:

Phosphofructokinase proteins

•400• 31

Pro Ser Asn Cys Gly Leu Glu Glu Lys Ile Ala Asn Leu Gly Ser Cys

1

5

10

15

Asn Asp Ser Lys Leu Glu Phe Arg Ser Phe Trp Glu Leu Ile Gly Glu

20

25

30

Ala Ala Lys Ser Val Lys Leu

35

•210• 22

•211• 10

•212• PRT

•213• Unknown Organism

•220•

•223• Description of Unknown Organism: PH domain

proteins profile

<400> 22

Pro Ser Asn Cys Gly Leu Glu Glu Lys Ile
1 5 10

<210> 23

<211> 45

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Myotoxins
protein

<400> 23

Gln Gln Leu Pro His Leu Met Pro Ser Asn Cys Gly Leu Glu Lys
1 5 10 15

Ile Ala Asn Leu Gly Ser Cys Asn Asp Ser Lys Leu Glu Phe Arg Ser
20 25 30

Phe Trp Glu Leu Ile Gly Glu Ala Ala Lys Ser Val Lys
35 40 45

<210> 24

<211> 17

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism:
Phosphatidylinositol-specific phospholipase X

<400> 24

Met Pro Ser Asn Cys Gly Leu Glu Glu Lys Ile Ala Asn Leu Gly Ser

1 5 10 15

Cys

<210> 25

<211> 45

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Glypicans
protein

<400> 25

Met Gly Gly Cys Arg Ser Ala Asn Ala Glu Asp Ala Gln Glu Phe Ser
1 5 10 15

Asp Val Glu Arg Ala Ile Glu Thr Leu Ile Lys Asn Phe His Gln Tyr
20 25 30

Ser Val Glu Gly Gly Lys Glu Thr Leu Thr Pro Ser Glu
35 40 45

<210> 26

<211> 10

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Membrane attack
complex components/perforin

<400> 26

Ile Lys Asn Phe His Gln Tyr Ser Val Glu
1 5 10

0210> 27

0211> 44

0212> PRT

0213> Unknown Organism

0220>

0223> Description of Unknown Organism: Urease nickel
ligands protein

0400> 27

Thr Leu Ile Lys Asn Phe His Gln Tyr Ser Val Glu Gly Gly Lys Glu
1 5 10 15

Thr Leu Thr Pro Ser Glu Leu Arg Asp Leu Val Thr Gln Gln Leu Pro
20 25 30

His Leu Met Pro Ser Asn Cys Gly Leu Glu Glu Lys
35 40

0210> 28

0211> 13

0212> PRT

0213> Unknown Organism

0220>

0223> Description of Unknown Organism: Phosphoglycerate
mutase family phosphohistidi

0400> 28

Gln Glu Phe Ser Asp Val Glu Arg Ala Ile Glu Thr Leu
1 5 10

0210> 29

0211> 10

0212> PRT

213 Unknown Organism

220

223 Description of Unknown Organism: Ribosomal protein
L23 protein

400 29

Glu Leu Arg Asp Leu Val Thr Gln Gln Leu
1 5 10

210 30

211 41

212 PRT

213 Unknown Organism

220

223 Description of Unknown Organism:
2'-5'-oligoadenylate synthetases protein

400 30

Leu Glu Glu Lys Ile Ala Asn Leu Gly Ser Cys Asn Asp Ser Lys Leu
1 5 10 15

Glu Phe Arg Ser Phe Trp Glu Leu Ile Gly Glu Ala Ala Lys Ser Val
20 25 30

Lys Leu Glu Arg Pro Val Arg Gly His
35 40

210 31

211 24

212 PRT

213 Unknown Organism

220

223 Description of Unknown Organism: Formate and

nitrite transporters protein

<400> 31

Asp Leu Val Thr Gln Gln Leu Pro His Leu Met Pro Ser Asn Cys Gly
1 5 10 15

Leu Glu Glu Lys Ile Ala Asn Leu
20

<210> 32

<211> 34

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Glycoprotein
hormones beta chain protein

<400> 32

Gln Gln Cys Arg Ser Ala Asn Ala Glu Asp Ala Gln Glu Phe Ser Asp
1 5 10 15

Val Glu Arg Ala Ile Glu Thr Leu Ile Lys Asn Phe His Gln Tyr Ser
20 25 30

Val Glu

<210> 33

<211> 21

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Vinculin family
talin-binding region protein

<400> 33

Lys Glu Thr Leu Thr Pro Ser Glu Leu Arg Asp Leu Val Thr Gln Gln
1 5 10 15

Leu Pro His Leu Met
20

<210> 34

<211> 40

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Beta-lactamases
clas B protein

<400> 34

Ile Glu Thr Leu Ile Lys Asn Phe His Gln Tyr Ser Val Glu Gly Gly
1 5 10 15

Lys Glu Thr Leu Thr Pro Ser Glu Leu Arg Asp Leu Val Thr Gln Gln
20 25 30

Leu Pro His Leu Met Pro Ser Asn
35 40

<210> 35

<211> 21

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Heat shock hsp20
protein family profile

4400 35

Leu Glu Phe Arg Ser Phe Trp Glu Leu Ile Gly Glu Ala Ala Lys Ser
1 5 10 15

Val Lys Leu Glu Arg
20

4210 36

4211 35

4212 PRT

4213 Unknown Organism

4220

4223 Description of Unknown Organism:

Hydroxymethylglutaryl-coenzyme A lyase protein

4400 36

Met Gly Gly Cys Arg Ser Ala Asn Ala Glu Asp Ala Gln Glu Phe Ser
1 5 10 15

Asp Val Glu Arg Ala Ile Glu Thr Leu Ile Lys Asn Phe His Gln Tyr
20 25 30

Ser Val Glu
35

4210 37

4211 294

4212 DNA

4213 Mus sp.

4400 37

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ggtgaccagg tcccgtagct cagaaggggt cagcgtctcc ttcccaccct ccacggagta 240

ctgggtgaaag ttcttgatga ggggtctcaat ggcctctccc acatcactga attc

294

0210> 38

0211> 43

0212> PPT

0213> Homo sapiens

0400> 38

Val Glu Arg Ala Ile Glu Thr Leu Ile Lys Asn Phe His Gln Tyr Ser

1

5

10

15

Val Glu Gly Gly Lys Glu Thr Leu Thr Pro Ser Glu Leu Arg Asp Leu

20

25

30

Val Thr Gln Gln Leu Pro His Leu Met Pro Ser

35

40

0210> 39

0211> 44

0212> PPT

0213> Homo sapiens

0400> 39

Asn Cys Gly Leu Glu Glu Lys Ile Ala Asn Leu Gly Ser Cys Asn Asp

1

5

10

15

Ser Lys Leu Glu Phe Arg Ser Phe Trp Glu Leu Ile Gly Glu Ala Ala

20

25

30

Lys Ser Val Lys Leu Glu Arg Pro Val Arg Gly His

35

40

0210> 40

0211> 44

0212> PPT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Consensus
sequence

<400> 40

Asn Cys Gly Leu Glu Glu Lys Ile Ala Asn Leu Gly Ser Cys Asn Asp
1 5 10 15

Ser Lys Leu Glu Phe Arg Ser Phe Trp Glu Leu Ile Gly Glu Ala Ala
20 25 30

Lys Ser Val Lys Leu Glu Arg Pro Val Arg Gly His
35 40

<210> 41

<211> 41

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: gi/4139958/pdb/1MHO

<400> 41

Glu Lys Ala Val Val Ala Leu Ile Asp Val Phe His Gln Tyr Ser Gly
1 5 10 15

Arg Glu Gly Asp Lys His Lys Leu Lys Lys Ser Glu Leu Lys Glu Leu
20 25 30

Ile Asn Asn Glu Leu Ser His Phe Leu
35 40

<210> 42

<211> 41

0212 PRT

0213 Unknown Organism

0220

0223 Description of Unknown Organism: Protein MRP-126

0400 42

Glu Lys Ala Ile Asp Val Ile Ile Asp Val Phe His Gln Tyr Ser Arg

1

5

10

15

Arg Glu Gly Asp Lys Asp Thr Leu Thr Arg Lys Glu Leu Lys Leu Leu

20

25

30

Ile Glu Lys Gln Leu Ala Asn Tyr Leu

35

40

0210 43

0211 41

0212 PRT

0213 Unknown Organism

0220

0223 Description of Unknown Organism: ICTACALCIN

0400 43

Gln Lys Gly Met Ala Leu Leu Ile Ser Thr Phe His Lys Tyr Ser Gly

1

5

10

15

Lys Glu Gly Asp Lys Cys Thr Leu Thr Lys Gly Glu Leu Lys Asp Leu

20

25

30

Ile Thr Lys Glu Leu Gly Gly Ala Phe

35

40

0210 44

0211 41

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: CALGRANULIN B

<400> 44

Glu Ser Ser Ile Glu Thr Ile Ile Asn Ile Phe His Gln Tyr Ser Val
1 5 10 15

Arg Leu Gly His Tyr Asp Thr Leu Ile Gln Lys Glu Phe Lys Gln Leu
20 25 30

Val Gln Lys Glu Leu Pro Asn Phe Leu
35 40

<210> 45

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Consensus
sequence

<400> 45

Ile Phe His Tyr Ser Gly Leu Glu Leu Leu
1 5 10

<210> 46

<211> 41

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: CALGRANULIN B

<400> 46

Glu Arg Ser Ile Thr Thr Ile Ile Asp Thr Phe His Gln Tyr Ser Arg
1 5 10 15

Lys Glu Gly His Pro Asp Thr Leu Ser Lys Lys Glu Phe Arg Gln Met
20 25 30

Val Glu Ala Gln Leu Ala Thr Phe Met
35 40

<210> 47

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Consensus
sequence

<400> 47

Glu Ile Phe His Gln Tyr Ser Gly Leu Glu Leu
1 5 10

<210> 48

<211> 44

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Alignment
sequence

<400> 48

Leu Glu Lys Ala Ile Glu Thr Ile Ile Asn Val Phe His Gln Tyr Ser
1 5 10 15

Gly Arg Glu Gly Asp Lys Asp Thr Leu Ser Lys Lys Glu Leu Lys Glu
20 25 30

Leu Leu Glu Lys Glu Leu Pro Asn Phe Leu Lys Asn
35 40